

SEQ ID NO: 12 (searched SEQ ID NO: 11, has mismatch therefore SEQ ID NO: 11).

RESULT 11

HSU70323

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N., Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G., Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R., Figueroa,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in

spinocerebellar ataxia type 2  
JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd., Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source 1. .4481  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/map="12q24.1"  
gene 163. .4101  
/gene="SCA2"  
CDS 163. .4101  
/gene="SCA2"  
/standard\_name="spinocerebellar ataxia type 2"  
/codon\_start=1  
/product="ataxin-2"  
/protein\_id="AAB19200.1"  
/db\_xref="GI:1679684"

/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRS LQRPARRSGRGGGG

AAPGPYP SAAPPPPGPGPPPSRQSSPPSASDCFGSNGNGGGA FRPGSRRL LGLGGPPR

PFVVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRP ACEPVYGPLT



SEQ ID NO: 1

RESULT 2

HSU70323

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N.,  
Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G.,  
Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R.,  
Figueroa,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in  
spinocerebellar ataxia type 2

JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd.,  
Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source

1. .4481

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="12"

/map="12q24.1"

gene

163. .4101

/gene="SCA2"

CDS

163. .4101

/gene="SCA2"

/standard\_name="spinocerebellar ataxia type 2"

/codon\_start=1

/product="ataxin-2"

/protein\_id="AAB19200.1"

/db\_xref="GI:1679684"

/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRSRQRPARRSGRGGGG  
AAPGPYPSPAAPPPPGPGPPPSRQSSPPSASDCFGSNGNGGGAFRPGSRRLGLGGPPR  
PFVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRPACFPVYGPLT  
MSLKPQQQQQQQQQQQQQQQQQQQQPPPAANVRKPGSGLLASPAAPSPSSSSV  
SSSSATAPSSVVAATSGGGRPGLGRGRNSNKGLPQSTISFDGIYANMRMVHILTSVVG  
SKCEVQVKNGGIYEGVFKTYSKCDLVLDAAHEKSTESSSGPKREEIMESILFKCSDF  
VVVQFKDMDSSYAKRDAFTDSAISAKVNGEHKEKDLEPWDAGELTANEELEALENDVS  
NGWDPNDMFRYNEENYGVVSTYDSSLSSYTVPLERDNSEEFKREARANQLAEIESS  
AQYKARVALENDDRSEBEKYTAVQRNSSEREHGSINTRENKYIPPGQRNREVISWGSG  
RQNSPRMGQPGSGSMPSRSTSTSDFNPNSSGSDQRVVNGGVPWPSPCPSPPSRPPSRY  
QSGPNSLPPRAATPTRPPSRPPSRPPSHPSAHGSPAPVSTMPKRMSSEGPPRMSP  
KAQRHPRNHRVSAGRGSISSGLEFVSHNPPSEAAATPPVARTSPSGGTWSSVSGVPRL  
SPKTHRPRSPRQNSIGNTPSGPVLASPAQAGIIPTEAVAMPIPAASPTPASPNRAVT  
PSSEAKDSRLQDQRQNSPAGNKENIKPNETSPSFSKAENKGISPVVSEHRKQIDDLKK  
FKNDFRLQPSSTSESMDQLLNKNREGEKSRDLIKDIEPSAKDSFIENSSNCTSGSS  
KPNSPSISPSILSNTEHKRGPEVTSQGVQTSPPACKQEKDDKEEKDAAEQVRKSTLN  
PNAKEFNPRSFSQPKPSTTPTSPRPQAQPSPSMVGHQOPTPVYTQPVCFAPNMMYPVP  
VSPGVQPLYPIPMTPMPVNQAKTYRAVPNMPQQRQDQHHQSAMMHPASAAGPPIAATP  
PAYSTQYVAYSPQQFPNQPLVQHVPHYQSQHPHYVSPVIQGNARMMAPTHAQPGLV  
SSATQYGAHEQTHAMYACPKLPYNKETSPSFYFAISTGSLAQYAHNPATLHPHTPHP  
QPSATPTGQQQSQHGGSHAPSPVQHHQHQAALHLASPPQQQSAIYHAGLAPTTPSM

TPASNTQSPQNSFPAAQQTVFTIHPSHVQPAYTNPPHMAHVPQAHVQSGMVPSHPTAH  
APMMLMTTQPPGGPQAALAQSAEQPIPVSTTAHFPYMTGPSVQAHHQQL"  
BASE COUNT 1144 a 1380 c 1014 g 943 t  
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 4481;  
Best Local Similarity 100.0%; Pred. No. 0.044;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctccgcctcagactggttttggtag 24  
|||  
Db 375 CTCCGCCTCAGACTGTTTGGTAG 398

SEQ ID NO: 2

RESULT 4

HSU70323/c

LOCUS HSU70323 4481 bp mRNA PRI 20-NOV-1996

DEFINITION Human ataxin-2 (SCA2) mRNA, complete cds.

ACCESSION U70323

VERSION U70323.1 GI:1679683

KEYWORDS .

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4481)

AUTHORS Pulst,S.-M., Nechiporuk,A., Nechiporuk,T., Gispert,S., Chen,X.-N., Lopes-Cendes,I., Pearlman,S., Starkman,S., Orozco-Diaz,G., Lunkes,A., DeJong,P., Rouleau,G.A., Auburger,G., Korenberg,J.R., Figueroa,C. and Sahba,S.

TITLE Moderate expansion of a normally biallelic trinucleotide repeat in spinocerebellar ataxia type 2

JOURNAL Nature Genet. 14 (3), 269-276 (1996)

MEDLINE 97051920

REFERENCE 2 (bases 1 to 4481)

AUTHORS Pulst,S.-M.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-1996) Medicine, Cedars-Sinai, 8700 Beverly Blvd., Los Angeles, CA 90048, USA

FEATURES Location/Qualifiers

source

1. .4481  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/map="12q24.1"

gene

163. .4101  
/gene="SCA2"

CDS

163. .4101  
/gene="SCA2"  
/standard\_name="spinocerebellar ataxia type 2"  
/codon\_start=1  
/product="ataxin-2"  
/protein\_id="AAB19200.1"  
/db\_xref="GI:1679684"  
/translation="MRSAAAAPRSPAVATESRRFAAARWPGWRSRQPARRSRGGGG  
AAPGPYPYSAAPPPPGPGPPSRQSSPPSASDCFGSNGNGGGAFRPGSRRLGLGGPPR  
PFVVVLLPLASPGAPPAAPTRASPLGARASPPRSGVSLARPAPGCPRPACEPVYGPLT  
MSLKPQQQQQQQQQQQQQQQQQQQQPPPAANVRKPGGSGLLASPAAPSPSSSSV  
SSSSATAPSSVVAATSGGGRPGLGRGRNSNKGLPQSTISFDGIYANMRMHILTSVVG  
SKCEVQVKNGGIYEGVFKTYSKCDLVLDAAHEKSTESSGPKREEIMESILFKCSDF  
VVVQFKDMDSSYAKRDAFTDSAISAKVNGEHKEKDLEPWDAGELTANEELEALENDVS  
NGWDPNDMFRYNEENYGVVSTYDSSLSSYTVPLERDNSEEFKREARANQLAEEIESS  
AQYKARVALENDDRSEEEKYTAVQRNSSEREHGSINTRENKYIPPGQRNREVISWGSG  
RQNSPRMGQPGSGSMPSRSTSHTSDFNPNSGSDQRVVNGGVPWPSPCPSRPPSRYP  
QSGPNSLPRAATPTRPPSRPPSRPPSHPSAHGSPAPVSTMPKRMSSEGPMPSP  
KAQRHPRNHRVSAGRSISSGLEFVSHNPPSEATPPVARTSPSGGTWSSVVGVPRL  
SPKTHRPRSPRQNSIGNTPSGPVLASPAQAGIIPTEAVAMPIPAASPTPASPNRAVT  
PSSEAKDSRLQDQRQNSPAGNKENIKPNETSPSFSKAENKGISPVVSEHRKQIDDLKK  
FKNDFRLQPSSTSESDQLLNKNREGEKSRDLIKDKIEPSAKDSFIENSSNCTSGSS  
KPNSPSISPSILSNTEHKGPEVTSQGVQTSSPACKQEKDDKEEKDAAEQVRKSTLN  
PNAKEFNPRSFSPKPTSTPTSPRPQAQSPSMVGHQOPTPVYTPVCFAPNMMYPVP  
VSPGVQPLYPIPMTPMPVNQAKTYRAVPNMPQQRQDQHHQSAMMHPASAAGPPIAATP  
PAYSTQYVAYSPQQFPNQPLVQHVPYQSQHPHYSPVVIQGNARMAPPHTHAQPLVS  
SSATQYGAHEQTHAMYACPKLPYNKETSPSFYFAISTGSLAQQYAHNPATLHPHTPHP

QPSATPTGQQSQHGGSHAPSPVQHHQHQAALHLASPOQQSAIYHAGLAPTPPSM  
TPASNTQSPQNSFPAAQQTFTIHPSHVQPAYTNPPHMAHVPQAHVQSGMVP SHPTAH  
APMMLMTTQPPGGPQAALAQSALQPIPVSTTAHFPYMTHTPSVQAHHQQQL"

BASE COUNT      1144 a    1380 c    1014 g      943 t  
ORIGIN

Query Match                    100.0%; Score 20; DB 9; Length 4481;  
Best Local Similarity    100.0%; Pred. No. 77;  
Matches    20; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy            1 gtggccgaggacgaggagac 20  
              |||||  
Db        833 GTGGCCGAGGACGAGGAGAC 814